SEQUENCE LISTING

<110> Turner, C. Alexander Jr.
        Hilbun, Erin
        Donoho, Gregory
        Scoville, John
        Wattler,. Frank
        Friedrich, Glenn
        Abuin, Alejandro
        Zambrowicz, Brian
        Sands, Arthur T.

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Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
        210                 215                 220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                245                 250                 255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
            260                 265                 270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
            275                 280                 285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
        290                 295                 300
Tyr Glu Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
305                 310                 315                 320
```

7

```
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
            325                     330                 335
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
            340                     345                 350
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
            355                     360                 365
Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
    370                 375                 380
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
385                 390                 395                 400
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
            405                 410                 415
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
            420                 425                 430
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
            435                 440                 445
Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
    450                 455                 460
Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
465                 470                 475                 480
Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
            485                 490                 495
Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
            500                 505                 510
Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
            515                 520                 525
Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
    530                 535                 540
Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
545                 550                 555                 560
Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
            565                 570                 575
Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
            580                 585                 590
Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
            595                 600                 605
Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
    610                 615                 620
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
625                 630                 635                 640
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
            645                 650                 655
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
            660                 665                 670
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
            675                 680                 685
Asn Cys Asp Ala Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu
    690                 695                 700
Ser Phe Lys Asp His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr
705                 710                 715                 720
Asp Arg Ser Asn Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys
            725                 730                 735
Tyr Gly Asp Arg Arg Phe Trp Asn Ala Val Ser Phe Tyr Thr Glu Ala
            740                 745                 750
Ser Tyr Leu His Phe Pro Thr Phe His Ala Glu Phe Ser Ala Asp Ile
    755                 760                 765
```

8

```
Ser Phe Phe Phe Lys Thr Thr Ala Leu Ser Gly Val Phe Leu Glu Asn
    770                 775                 780
Leu Gly Ile Lys Asp Phe Ile Arg Leu Glu Ile Ser Ser Pro Ser Glu
785                 790                 795                 800
Ile Thr Phe Ala Ile Asp Val Gly Asn Gly Pro Val Glu Leu Val Val
                805                 810                 815
Gln Ser Pro Ser Leu Leu Asn Asp Asn Gln Trp His Tyr Val Arg Ala
            820                 825                 830
Glu Arg Asn Leu Lys Glu Thr Ser Leu Gln Val Asp Asn Leu Pro Arg
            835                 840                 845
Ser Thr Arg Glu Thr Ser Glu Glu Gly His Phe Arg Leu Gln Leu Asn
        850                 855                 860
Ser Gln Leu Phe Val Gly Gly Thr Ser Ser Arg Gln Lys Gly Phe Leu
865                 870                 875                 880
Gly Cys Ile Arg Ser Leu His Leu Asn Gly Gln Lys Met Asp Leu Glu
                885                 890                 895
Glu Arg Ala Lys Val Thr Ser Gly Val Arg Pro Gly Cys Pro Gly His
            900                 905                 910
Cys Ser Ser Tyr Gly Ser Ile Cys His Asn Gly Gly Lys Cys Val Glu
        915                 920                 925
Lys His Asn Gly Tyr Leu Cys Asp Cys Thr Asn Ser Pro Tyr Glu Gly
    930                 935                 940
Pro Phe Cys Lys Lys Glu Val Ser Ala Val Phe Glu Ala Gly Thr Ser
945                 950                 955                 960
Val Thr Tyr Met Phe Gln Glu Pro Tyr Pro Val Thr Lys Asn Ile Ser
                965                 970                 975
Leu Ser Ser Ser Ala Ile Tyr Thr Asp Ser Ala Pro Ser Lys Glu Asn
            980                 985                 990
Ile Ala Leu Ser Phe Val Thr Thr Gln Ala Pro Ser Leu Leu Leu Phe
        995                 1000                1005
Ile Asn Ser Ser Ser Gln Asp Phe Val Val Val Leu Leu Cys Lys Asn
    1010                1015                1020
Gly Ser Leu Gln Val Arg Tyr His Leu Asn Lys Glu Glu Thr His Val
1025                1030                1035                1040
Phe Thr Ile Asp Ala Asp Asn Phe Ala Asn Arg Arg Met His His Leu
                1045                1050                1055
Lys Ile Asn Arg Glu Gly Arg Glu Leu Thr Ile Gln Met Asp Gln Gln
            1060                1065                1070
Leu Arg Leu Ser Tyr Asn Phe Ser Pro Glu Val Glu Phe Arg Val Ile
            1075                1080                1085
Arg Ser Leu Thr Leu Gly Lys Val Thr Glu Asn Leu Gly Leu Asp Ser
        1090                1095                1100
Glu Val Ala Lys Ala Asn Ala Met Gly Phe Ala Gly Cys Met Ser Ser
1105                1110                1115                1120
Val Gln Tyr Asn His Ile Ala Pro Leu Lys Ala Ala Leu Arg His Ala
                1125                1130                1135
Thr Val Ala Pro Val Thr Val His Gly Thr Leu Thr Glu Ser Ser Cys
            1140                1145                1150
Gly Phe Met Val Asp Ser Asp Val Asn Ala Val Thr Thr Val His Ser
        1155                1160                1165
Ser Ser Asp Pro Phe Gly Lys Thr Asp Glu Arg Glu Pro Leu Thr Asn
    1170                1175                1180
Ala Val Arg Ser Asp Ser Ala Val Ile Gly Gly Val Ile Ala Val Val
1185                1190                1195                1200
Ile Phe Ile Ile Phe Cys Ile Ile Gly Ile Met Thr Arg Phe Leu Tyr
                1205                1210                1215
```

9

Gln His Lys Gln Ser His Arg Thr Ser Gln Met Lys Glu Lys Glu Tyr
            1220   1225   1230
Pro Glu Asn Leu Asp Ser Ser Phe Arg Asn Glu Ile Asp Leu Gln Asn
            1235   1240   1245
Thr Val Ser Glu Cys Lys Arg Glu Tyr Phe Ile
        1250   1255

<210> 5
<211> 108
<212> DNA
<213> homo sapiens

<400> 5
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ttaggattaa cagcgacaaa ctacctttgc aggaaacatg aatgctga   108

<210> 6
<211> 35
<212> PRT
<213> homo sapiens

<400> 6
Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser
 1   5   10   15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Leu Cys Arg Lys
            20   25   30
His Glu Cys
        35

<210> 7
<211> 753
<212> DNA
<213> homo sapiens

<400> 7
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ttaggattaa cagcgacaaa ctacaactgt gatgatccac tagcatccct gctctctcca   120
atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg   180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg   240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct   300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac   360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac   420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat   480
cccagtggga gattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt   540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact   600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag agatggggt cctgttccat   660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaagggag gctcgcccta   720
cacctcaatt tggtggtttg tagttctcct tga   753

<210> 8
<211> 250
<212> PRT
<213> homo sapiens

<400> 8
Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser

10

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          1                   5                   10                  15
      Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
                      20                  25                  30
      Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
                      35                  40                  45
      Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
                      50                  55                  60
      Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
      65                  70                  75                  80
      Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                      85                  90                  95
      Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
                      100                 105                 110
      Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
                      115                 120                 125
      Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
                      130                 135                 140
      His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
      145                 150                 155                 160
      Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                      165                 170                 175
      Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
                      180                 185                 190
      Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
                      195                 200                 205
      Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
                      210                 215                 220
      Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
      225                 230                 235                 240
      His Leu Asn Leu Val Val Cys Ser Ser Pro
                      245                 250

<210> 9
<211> 840
<212> DNA
<213> homo sapiens

<400> 9
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atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg   180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg   240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct   300
gactgggtga cgagttacag cctgatgttc agtgacacag acgcaactg gaaacagtac   360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac   420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat   480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt   540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact   600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat   660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaagggag gctcgcccta   720
cacctcaatt tgggtgacag caaagcgcgg ctaagcactt gccctctgcc accctgggca   780
gcctcctgga tgaccagcac tggcactygg tcctcattga gcgggtgggc aagcaggtga   840

<210> 10
<211> 279
<212> PRT
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11

<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(279)
<223> Xaa = Any Amino Acid

<400> 10

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Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser
 1               5                  10                  15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
            35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
        50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
            115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
     130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145                 150                 155                 160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                165                 170                 175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180                 185                 190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
            195                 200                 205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
     210                 215                 220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Thr Cys Pro Leu
                245                 250                 255
Pro Pro Trp Ala Ala Ser Trp Met Thr Ser Thr Gly Thr Xaa Ser Ser
            260                 265                 270
Leu Ser Gly Trp Ala Ser Arg
            275
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<210> 11
<211> 1749
<212> DNA
<213> homo sapiens

<400> 11

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atggctttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg    180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg ctccagatg    240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct    300
```

12

```
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac      360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac      420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat      480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt      540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact      600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat      660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta      720
cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgcccct gccaccctg      780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag      840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc      900
ttagacattg actatgagct tagttttgga ggaattccag taccaggaaa acctgggacc      960
tttttaaaga aaaacttcca tggatgcatc gaaaaccttt actacaatgg agtaaacata     1020
attacctgg ctaagagacg aaagcatcag atctatactg tgggcaatgt cacttttcc     1080
tgctccgaac cacagattgt gcccatcaca tttgtyaact ccagcggcag ctatttgctg     1140
ctgcccggca cccccccaaat tgatgggctc tcagtgagtt tccagtttcg aacatggaac     1200
aaggatggtc tgcttctgtc cacagagctg tctgagggct cgggaacccct gctgctgagc     1260
ctggagggtg gaatcctgag actcgtgatt cagaaaatga cagaacgcgt agctgaaatc     1320
ctcacaggca gcaacttgaa tgatggcctg tggcactcgg ttagcatcaa cgccaggagg     1380
aaccgcatca cgctcactct ggatgatgaa gcagcacccc cggctccaga cagcacttgg     1440
gtgcagattt attctggaaa tagctactat tttggaggtg tttgccaaac tactgtgaac     1500
atggaggaag ctgctcccag tcctggacta ccttctattg taactgcagt gacacaagtt     1560
acactggtgc cacctgccac aactccatct acgagcaatc ctgcgaggtg tacaggcacc     1620
aggggaatac agccggcttc ttctacatcg actcagatgg cagcggccca ctgggacctc     1680
tccaggtgta ctgcaatatc actgaggaca agatctggac atcagtgcag cacaacaata     1740
cagagctga                                                            1749
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<210> 12
<211> 582
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(582)
<223> Xaa = Any Amino Acid

<400> 12

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Met Asp Ser Leu Pro Arg Leu Thr Ser Val Leu Thr Leu Leu Phe Ser
 1               5                  10                  15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20              25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
            35              40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
        50              55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65              70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
            115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
        130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
```

13

```
145                    150                    155                    160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                   165                    170                    175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
                   180                    185                    190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
              195                    200                    205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
         210                    215                    220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                    230                    235                    240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                   245                    250                    255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
                   260                    265                    270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
              275                    280                    285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
         290                    295                    300
Tyr Glu Leu Ser Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr
305                    310                    315                    320
Phe Leu Lys Lys Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn
                   325                    330                    335
Gly Val Asn Ile Ile Xaa Leu Ala Lys Arg Arg Lys His Gln Ile Tyr
                   340                    345                    350
Thr Val Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
              355                    360                    365
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
         370                    375                    380
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
385                    390                    395                    400
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
                   405                    410                    415
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
                   420                    425                    430
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
              435                    440                    445
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
         450                    455                    460
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
465                    470                    475                    480
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Val Cys Gln
                   485                    490                    495
Thr Thr Val Asn Met Glu Glu Ala Ala Pro Ser Pro Gly Leu Pro Ser
              500                    505                    510
Ile Val Thr Ala Val Thr Gln Val Thr Leu Val Pro Pro Ala Thr Thr
         515                    520                    525
Pro Ser Thr Ser Asn Pro Ala Arg Cys Thr Gly Thr Arg Gly Ile Gln
         530                    535                    540
Pro Ala Ser Ser Thr Ser Thr Gln Met Ala Ala Ala His Trp Asp Leu
545                    550                    555                    560
Ser Arg Cys Thr Ala Ile Ser Leu Arg Thr Arg Ser Gly His Gln Cys
                   565                    570                    575
Ser Thr Thr Ile Gln Ser
              580
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14

<210> 13
<211> 1605
<212> DNA
<213> homo sapiens

<400> 13
atggattctt taccacggct gaccagcgtt ttgactttgc tgttctctgg cttgtggcat   60
ttaggattaa cagcgacaaa ctacaactgt gatgatccac tagcatccct gctctctcca   120
atggctttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg   180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg   240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct   300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac   360
aaacaagaag acagcatctg gaccttttgca ggaaacatga atgctgacag cgtggtgcac   420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat   480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt   540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact   600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag agatgggggt cctgttccat   660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaagggggag gctcgcccta   720
cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg   780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag   840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc   900
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atcacatttg tyaactccag cggcagctat ttgctgctgc ccggcacccc ccaaattgat   1020
gggctctcag tgagtttcca gtttcgaaca tggaacaagg atggtctgct tctgtccaca   1080
gagctgtctg agggctcggg aaccctgctg ctgagcctgg agggtggaat cctgagactc   1140
gtgattcaga aaatgacaga acgcgtagct gaaatcctca caggcagcaa cttgaatgat   1200
ggcctgtggc actcggttag catcaacgcc aggaggaacc gcatcacgct cactctggat   1260
gatgaagcag cacccccggc tccagacagc acttgggtgc agatttattc tggaaatagc   1320
tactattttg gaggtgtttg ccaaactact gtgaacatgg aggaagctgc tcccagtcct   1380
ggactacctt ctattgtaac tgcagtgaca caagttacac tggtgccacc tgccacaact   1440
ccatctacga gcaatcctgc gaggtgtaca ggcaccaggg aatacagcc ggcttcttct   1500
acatcgactc agatggcagc ggcccactgg gacctctcca ggtgtactgc aatatcactg   1560
aggacaagat ctggacatca gtgcagcaca acaatacaga gctga   1605

<210> 14
<211> 534
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(534)
<223> Xaa = Any Amino Acid

<400> 14
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 1   5   10   15
Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20   25   30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Asp
            35   40   45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
        50   55   60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65   70   75   80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg

15

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                        85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
                100                 105                 110  ·
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
        115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145                 150                 155                 160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                165                 170                 175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
        180                 185                 190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
        195                 200                 205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210                 215                 220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                245                 250                 255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
                260                 265                 270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
                275                 280                 285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
                290                 295                 300
Tyr Glu Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
305                 310                 315                 320
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
                325                 330                 335
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
                340                 345                 350
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
                355                 360                 365
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
        370                 375                 380
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
385                 390                 395                 400
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
                405                 410                 415
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
                420                 425                 430
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Val Cys Gln
        435                 440                 445
Thr Thr Val Asn Met Glu Glu Ala Ala Pro Ser Pro Gly Leu Pro Ser
    450                 455                 460
Ile Val Thr Ala Val Thr Gln Val Thr Leu Val Pro Pro Ala Thr Thr
465                 470                 475                 480
Pro Ser Thr Ser Asn Pro Ala Arg Cys Thr Gly Thr Arg Gly Ile Gln
                485                 490                 495
Pro Ala Ser Ser Thr Ser Thr Gln Met Ala Ala Ala His Trp Asp Leu
        500                 505                 510
Ser Arg Cys Thr Ala Ile Ser Leu Arg Thr Arg Ser Gly His Gln Cys
        515                 520                 525
Ser Thr Thr Ile Gln Ser
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16

530

<210> 15
<211> 2238
<212> DNA
<213> homo sapiens

<400> 15
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atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg     180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg     240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct     300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac     360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac     420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat     480
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cacctcaatt tgggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg     780
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attracctgg ctaagagacg aaagcatcag atctatactg tgggcaatgt cactttttcc    1080
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aaggatggtc tgcttctgtc cacagagctg tctgagggct cgggaaccct gctgctgagc    1260
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cacattgatc tgtgtagcat caaagacagg tgtttgccaa actactgtga acatggagga    1680
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taccactgca ggaggtcccg cctgctcaac acgccggatg gaacaccatt tacctggtgg    2100
attgggcggt ccaatgaaag gcacccttac tggggaggtt cccctcctgg ggtccagcag    2160
tgtgagtgtg gcctagacga gagctgcctg gacattcagc acttttgcaa ttgcgacgct    2220
gacaaggatg aatggtaa                                                 2238
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<210> 16
<211> 745
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(745)
<223> Xaa = Any Amino Acid

17

<400> 16

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Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20              25              30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
            35              40              45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50              55              60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65              70              75              80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
            85              90              95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100             105             110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
    115             120             125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130             135             140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145             150             155             160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
            165             170             175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180             185             190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
    195             200             205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210             215             220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225             230             235             240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
            245             250             255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
            260             265             270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
    275             280             285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
    290             295             300
Tyr Glu Leu Ser Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr
305             310             315             320
Phe Leu Lys Lys Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn
            325             330             335
Gly Val Asn Ile Ile Xaa Leu Ala Lys Arg Arg Lys His Gln Ile Tyr
            340             345             350
Thr Val Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
    355             360             365
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
    370             375             380
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
385             390             395             400
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
            405             410             415
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
            420             425             430
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
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18

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                435                     440                     445
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
    450                     455                     460
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
465                     470                     475                     480
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
                485                     490                     495
Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
                500                     505                     510
Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
                515                     520                     525
Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
                530                     535                     540
Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
545                     550                     555                     560
Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
                565                     570                     575
Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
                580                     585                     590
Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
                595                     600                     605
Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
                610                     615                     620
Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
625                     630                     635                     640
Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
                645                     650                     655
Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
                660                     665                     670
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
                675                     680                     685
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
                690                     695                     700
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
705                     710                     715                     720
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
                725                     730                     735
Asn Cys Asp Ala Asp Lys Asp Glu Trp
                740                     745


<210>  17
<211>  2094
<212>  DNA
<213>  homo sapiens


<400>  17
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atggcttttt ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg     180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg     240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct     300
gactgggtga cgagttacag cctgatgttc agtgacacag acgcaactg gaaacagtac     360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac     420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat     480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt     540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact     600
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19

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ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat      660
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cacctcaatt tggggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg      780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag      840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc      900
ttagacattg actatgaggg caatgtcact ttttcctgct ccgaaccaca gattgtgccc      960
atcacatttg tyaactccag cggcagctat ttgctgctgc ccggcacccc ccaaattgat     1020
gggctctcag tgagtttcca gtttcgaaca tggaacaagg atggtctgct tctgtccaca     1080
gagctgtctg agggctcggg aaccctgctg ctgagcctgg agggtggaat cctgagactc     1140
gtgattcaga aaatgacaga acgcgtagct gaaatcctca caggcagcaa cttgaatgat     1200
ggcctgtggc actcggttag catcaacgcc aggaggaacc gcatcacgct cactctggat     1260
gatgaagcag cacccccggc tccagacagc acttgggtgc agatttattc tggaaatagc     1320
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gacaggtgtt tgccaaacta ctgtgaacat ggaggaagct gctcccagtc ctggactacc     1560
ttctattgta actgcagtga cacaagttac actggtgcca cctgccacaa ctccatctac     1620
gagcaatcct gcgaggtgta caggcaccag gggaatacag ccggcttctt ctacatcgac     1680
tcagatggca gcggcccact gggacctctc caggtgtact gcaatatcac tgaggacaag     1740
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gagaagccct atgccatggc cttggactac ggggggcagca tggaacagct ggaggccgtg     1860
atcgacggct ctgagcactg tgagcaggag gtggcctacc actgcaggag gtcccgcctg     1920
ctcaacacgc cggatggaac accatttacc tggtggattg ggcggtccaa tgaaaggcac     1980
ccttactggg gaggttcccc tcctggggtc cagcagtgtg agtgtggcct agacgagagc     2040
tgcctggaca ttcagcactt ttgcaattgc gacgctgaca aggatgaatg gtaa           2094
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<210> 18
<211> 697
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(697)
<223> Xaa = Any Amino Acid

<400> 18

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Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
            20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
            35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
            115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
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20

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        145                    150                    155                    160
        Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                            165                    170                    175
        Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
                            180                    185                    190
        Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
                    195                    200                    205
        Phe Lys Ser Met Gln Gly Asp. Gly Val Leu Phe His Gly Glu Gly Gln
                    210                    215                    220
        Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
        225                    230                    235                    240
        His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                            245                    250                    255
        Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
                            260                    265                    270
        Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
                    275                    280                    285
        Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
                    290                    295                    300
        Tyr Glu Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
        305                    310                    315                    320
        Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
                            325                    330                    335
        Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
                            340                    345                    350
        Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
                    355                    360                    365
        Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
                    370                    375                    380
        Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
        385                    390                    395                    400
        Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
                            405                    410                    415
        Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
                            420                    425                    430
        Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
                    435                    440                    445
        Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
            450                    455                    460
        Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
        465                    470                    475                    480
        Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
                            485                    490                    495
        Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
                    500                    505                    510
        Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
                    515                    520                    525
        Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
            530                    535                    540
        Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
        545                    550                    555                    560
        Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
                            565                    570                    575
        Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
                    580                    585                    590
        Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
```

21

```
          595                    600                    605
Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
          610                    615         .            620
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
625                    630                    635                640
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
                    645                    650                    655
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
                    660                    665                    670
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
                    675                    680                    685
Asn Cys Asp Ala Asp Lys Asp Glu Trp                    .
          690                    695
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<400> 19
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tgacctggga acagagtaga gattacagca gtggccacgc agggaagata cggaagctct   300
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aaacaagaag acagcatctg gaccttgca ggaaacatga atgctgacag cgtggtgcac   420
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cccagtggga gattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt   540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact   600
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gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga acggatgcc   900
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tgctccgaac cacagattgt gcccatcaca tttgtyaact ccagcggcag ctatttgctg  1140
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cccttgcgtt gctatggtga ccgtgagtac aaaatcgaaa gaagctttct ctctgcatta    2400
catgagcaca agatgttctt actcccttat ccctttttcc tgcagtgtgc cctagtcttg    2460
aaaattatcc acatgtccag tgctttccca taccccactg aaaacgataa accatgttga    2520
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<210> 20
<211> 839
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(839)
<223> Xaa = Any Amino Acid

<400> 20

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Gly Leu Trp His Leu Gly Leu Thr Ala Thr Asn Tyr Asn Cys Asp Asp
        20                  25                  30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
        35                  40                  45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50                  55                  60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65                  70                  75                  80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85                  90                  95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
        100                 105                 110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
        115                 120                 125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
    130                 135                 140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145                 150                 155                 160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                165                 170                 175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180                 185                 190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
        195                 200                 205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
    210                 215                 220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225                 230                 235                 240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                245                 250                 255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
                260                 265                 270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
        275                 280                 285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
    290                 295                 300
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23

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Tyr Glu Leu Ser Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr
305                 310                 315                 320
Phe Leu Lys Lys Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn
                325                 330                 335
Gly Val Asn Ile Ile Xaa Leu Ala Lys Arg Arg Lys His Gln Ile Tyr
                340                 345                 350
Thr Val Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
                355                 360                 365
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr
    370                 375                 380
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
385                 390                 395                 400
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
                405                 410                 415
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
                420                 425                 430
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
    435                 440                 445
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
    450                 455                 460
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
465                 470                 475                 480
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
                485                 490                 495
Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
                500                 505                 510
Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
    515                 520                 525
Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
    530                 535                 540
Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
545                 550                 555                 560
Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
                565                 570                 575
Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
    580                 585                 590
Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
    595                 600                 605
Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
    610                 615                 620
Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
625                 630                 635                 640
Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
                645                 650                 655
Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
                660                 665                 670
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
    675                 680                 685
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
    690                 695                 700
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
705                 710                 715                 720
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
                725                 730                 735
Asn Cys Asp Ala Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu
                740                 745                 750
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24

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Ser Phe Lys Asp His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr
        755                 760                 765
Asp Arg Ser Asn Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys
        770                 775                 780
Tyr Gly Asp Arg Glu Tyr Lys Ile Glu Arg Ser Phe Leu Ser Ala Leu
785                 790                 795                 800
His Glu His Lys Met Phe Leu Leu Pro Tyr Pro Phe Ser Leu Gln Cys
            805                 810                 815
Ala Leu Val Leu Lys Ile Ile His Met Ser Ser Ala Phe Pro Tyr Pro
            820             825                 830
Thr Glu Asn Asp Lys Pro Cys
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<210> 21
<211> 2376
<212> DNA
<213> homo sapiens

<400> 21

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atggctttt  ccagttcctc agacctcact ggcactcaca gcccagctca actcaactgg     180
agagttggaa ctggcggttg gtccccagca gattccaatg ctcaacagtg gctccagatg     240
gacctgggaa acagagtaga gattacagca gtggccacgc agggaagata cggaagctct     300
gactgggtga cgagttacag cctgatgttc agtgacacag gacgcaactg gaaacagtac     360
aaacaagaag acagcatctg gacctttgca ggaaacatga atgctgacag cgtggtgcac     420
cacaagctat tgcactcagt gagagcccga tttgttcgct ttgtgcccct ggaatggaat     480
cccagtggga agattggcat gagagtcgag gtctacggat gttcctataa atcagacgtt     540
gctgactttg atggccgaag ctcacttctg tacaggttca atcagaagtt gatgagtact     600
ctcaaagatg tgatctccct gaagttcaag agcatgcaag gagatggggt cctgttccat     660
ggagaaggtc agcgtggaga ccacatcacc ttggaactcc agaaggggag gctcgcccta     720
cacctcaatt ggggtgacag caaagcgcgg ctcagcagca gcttgccctc tgccaccctg     780
ggcagcctcc tggatgacca gcactggcac tyggtcctca ttgagcgggt gggcaagcag     840
gtgaacttca cggtggacaa gcacacacag cacttccgca ccaagggcga gacggatgcc     900
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atcacatttg tyaactccag cggcagctat ttgctgctgc ccggcacccc ccaaattgat    1020
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gagctgtctg agggctcggg aaccctgctg ctgagcctgg agggtggaat cctgagactc    1140
gtgattcaga aaatgacaga acgcgtagct gaaatcctca caggcagcaa cttgaatgat    1200
ggcctgtggc actcggttag catcaacgcc aggaggaacc gcatcacgct cactctggat    1260
gatgaagcag caccccccggc tccagacagc acttgggtgc agatttattc tggaaatagc    1320
tactattttg gagggtgccc cgacaatctc accgattccc aatgtttaaa tcccattaag    1380
gctttccaag gctgcatgag gctcatcttt attgataacc agcccaagga cctcatttca    1440
gttcagcaag gttccctggg gaattttagt gatttacaca ttgatctgtg tagcatcaaa    1500
gacaggtgtt tgccaaacta ctgtgaacat ggaggaagct gctcccagtc ctggactacc    1560
ttctattgta actgcagtga cacaagttac actggtgcca cctgccacaa ctccatctac    1620
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ccttactggg gaggttcccc tcctggggtc cagcagtgtg agtgtggcct agacgagagc    2040
tgcctggaca ttcagcactt ttgcaattgc gacgctgaca aggatgaatg gacaaatgat    2100
actggctttc tttccttcaa agaccacttg cctgtcactc agatagttat cactgatacc    2160
gacagatcaa actcagaagc cgcttggaga attggtccct tgcgttgcta tggtgaccgt    2220
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gagtacaaaa tcgaaagaag ctttctctct gcattacatg agcacaagat gttcttactc   2280
ccttatccct tttcccccgca gtgtgcccta gtcttgaaaa ttatccacat gtccagtgct   2340
ttcccatacc ccactgaaaa cgataaacca tgttga   2376

<210> 22
<211> 791
<212> PRT
<213> homo sapiens

<220>
<221> VARIANT
<222> (1)...(791)
<223> Xaa = Any Amino Acid

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            20   25   30
Pro Leu Ala Ser Leu Leu Ser Pro Met Ala Phe Ser Ser Ser Ser Asp
        35   40   45
Leu Thr Gly Thr His Ser Pro Ala Gln Leu Asn Trp Arg Val Gly Thr
    50   55   60
Gly Gly Trp Ser Pro Ala Asp Ser Asn Ala Gln Gln Trp Leu Gln Met
65   70   75   80
Asp Leu Gly Asn Arg Val Glu Ile Thr Ala Val Ala Thr Gln Gly Arg
                85   90   95
Tyr Gly Ser Ser Asp Trp Val Thr Ser Tyr Ser Leu Met Phe Ser Asp
            100   105   110
Thr Gly Arg Asn Trp Lys Gln Tyr Lys Gln Glu Asp Ser Ile Trp Thr
            115   120   125
Phe Ala Gly Asn Met Asn Ala Asp Ser Val Val His His Lys Leu Leu
        130   135   140
His Ser Val Arg Ala Arg Phe Val Arg Phe Val Pro Leu Glu Trp Asn
145   150   155   160
Pro Ser Gly Lys Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr
                165   170   175
Lys Ser Asp Val Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg
            180   185   190
Phe Asn Gln Lys Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys
            195   200   205
Phe Lys Ser Met Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln
            210   215   220
Arg Gly Asp His Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu
225   230   235   240
His Leu Asn Leu Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro
                245   250   255
Ser Ala Thr Leu Gly Ser Leu Leu Asp Asp Gln His Trp His Xaa Val
            260   265   270
Leu Ile Glu Arg Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His
            275   280   285
Thr Gln His Phe Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp
    290   295   300
Tyr Glu Gly Asn Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro
305   310   315   320
Ile Thr Phe Val Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr

26

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                    325                      330                      335
Pro Gln Ile Asp Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn
                    340                      345                      350
Lys Asp Gly Leu Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr
                    355                      360                      365
Leu Leu Leu Ser Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys
                    370                      375                      380
Met Thr Glu Arg Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp
385                      390                      395                      400
Gly Leu Trp His Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr
                    405                      410                      415
Leu Thr Leu Asp Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp
                    420                      425                      430
Val Gln Ile Tyr Ser Gly Asn Ser Tyr Tyr Phe Gly Gly Cys Pro Asp
                    435                      440                      445
Asn Leu Thr Asp Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly
                    450                      455                      460
Cys Met Arg Leu Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser
465                      470                      475                      480
Val Gln Gln Gly Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu
                    485                      490                      495
Cys Ser Ile Lys Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly
                    500                      505                      510
Ser Cys Ser Gln Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr
                    515                      520                      525
Ser Tyr Thr Gly Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys
545                      550                      555                      560
Glu Val Tyr Arg His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp
                    565                      570                      575
Ser Asp Gly Ser Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile
                    580                      585                      590
Thr Glu Asp Lys Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu
                    595                      600                      605
Thr Arg Val Arg Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu
                    610                      615                      620
Asp Tyr Gly Gly Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser
625                      630                      635                      640
Glu His Cys Glu Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu
                    645                      650                      655
Leu Asn Thr Pro Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser
                    660                      665                      670
Asn Glu Arg His Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln
                    675                      680                      685
Cys Glu Cys Gly Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys
                    690                      695                      700
Asn Cys Asp Ala Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu
705                      710                      715                      720
Ser Phe Lys Asp His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr
                    725                      730                      735
Asp Arg Ser Asn Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys
                    740                      745                      750
Tyr Gly Asp Arg Glu Tyr Lys Ile Glu Arg Ser Phe Leu Ser Ala Leu
                    755                      760                      765
His Glu His Lys Met Phe Leu Leu Pro Tyr Pro Phe Ser Leu Gln Cys
Ala Leu Val Leu Lys Ile Ile His Met Ser Ser Ala Phe Pro Tyr Pro
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27

770   775   780
Thr Glu Asn Asp Lys Pro Cys
785   790

<210> 23
<211> 3897
<212> DNA
<213> Homo sapiens

<400> 23
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actggcactc acagcccagc tcaactcaac tggagagttg gaactggcgg ttggtcccca   180
gcagattcca atgctcaaca gtggctccag atggacctgg gaaacagagt agagattaca   240
gcagtggcca cgcagggaag atacggaagc tctgactggg tgacgagtta cagcctgatg   300
ttcagtgaca caggacgcaa ctggaaacag tacaaacaag aagacagcat ctggaccttt   360
gcaggaaaca tgaatgctga cagcgtggtg caccacaagc tattgcactc agtgagagcc   420
cgatttgttc gctttgtgcc cctggaatgg aatcccagtg ggaagattgg catgagagtc   480
gaggtctacg gatgttccta taaatcagac gttgctgact ttgatggccg aagctcactt   540
ctgtacaggt tcaatcagaa gttgatgagt actctcaaag atgtgatctc cctgaagttc   600
aagagcatgc aaggagatgg ggtcctgttc catggagaag gtcagcgtgg agaccacatc   660
accttggaac tccagaaggg gaggctcgcc ctacacctca atttgggtga cagcaaagcg   720
cggctcagca gcagcttgcc ctctgccacc ctgggcagcc tcctggatga ccagcactgg   780
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cagctgaaca gccagttgtt tgtaggggga acgtcatcca gacagaaagg cttcctagga 2760

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<210> 24
<211> 1298
<212> PRT
<213> Homo sapiens

<400> 24

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Ile Ile Asp Asn Cys Asp Asp Pro Leu Ala Ser Leu Leu Ser Pro Met
            20                  25                  30
Ala Phe Ser Ser Ser Ser Asp Leu Thr Gly Thr His Ser Pro Ala Gln
            35                  40                  45
Leu Asn Trp Arg Val Gly Thr Gly Gly Trp Ser Pro Ala Asp Ser Asn
    50                  55                  60
Ala Gln Gln Trp Leu Gln Met Asp Leu Gly Asn Arg Val Glu Ile Thr
65                  70                  75                  80
Ala Val Ala Thr Gln Gly Arg Tyr Gly Ser Ser Asp Trp Val Thr Ser
                85                  90                  95
Tyr Ser Leu Met Phe Ser Asp Thr Gly Arg Asn Trp Lys Gln Tyr Lys
            100                 105                 110
Gln Glu Asp Ser Ile Trp Thr Phe Ala Gly Asn Met Asn Ala Asp Ser
            115                 120                 125
Val Val His His Lys Leu Leu His Ser Val Arg Ala Arg Phe Val Arg
    130                 135                 140
Phe Val Pro Leu Glu Trp Asn Pro Ser Gly Lys Ile Gly Met Arg Val
145                 150                 155                 160
Glu Val Tyr Gly Cys Ser Tyr Lys Ser Asp Val Ala Asp Phe Asp Gly
                165                 170                 175
Arg Ser Ser Leu Leu Tyr Arg Phe Asn Gln Lys Leu Met Ser Thr Leu
            180                 185                 190
Lys Asp Val Ile Ser Leu Lys Phe Lys Ser Met Gln Gly Asp Gly Val
            195                 200                 205
Leu Phe His Gly Glu Gly Gln Arg Gly Asp His Ile Thr Leu Glu Leu
    210                 215                 220
Gln Lys Gly Arg Leu Ala Leu His Leu Asn Leu Gly Asp Ser Lys Ala
225                 230                 235                 240
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29

Arg Leu Ser Ser Ser Leu Pro Ser Ala Thr Leu Gly Ser Leu Leu Asp
                  245   250   255
Asp Gln His Trp His Ser Val Leu Ile Glu Arg Val Gly Lys Gln Val
                  260   265   270
Asn Phe Thr Val Asp Lys His Thr Gln His Phe Arg Thr Lys Gly Glu
                  275   280   285
Thr Asp Ala Leu Asp Ile Asp Tyr Glu Leu Ser Phe Gly Gly Ile Pro
        290   295   300
Val Pro Gly Lys Pro Gly Thr Phe Leu Lys Lys Asn Phe His Gly Cys
305   310   315   320
Ile Glu Asn Leu Tyr Tyr Asn Gly Val Asn Ile Ile Asp Leu Ala Lys
                  325   330   335
Arg Arg Lys His Gln Ile Tyr Thr Val Gly Asn Val Thr Phe Ser Cys
                  340   345   350
Ser Glu Pro Gln Ile Val Pro Ile Thr Phe Val Asn Ser Ser Gly Ser
                  355   360   365
Tyr Leu Leu Leu Pro Gly Thr Pro Gln Ile Asp Gly Leu Ser Val Ser
        370   375   380
Phe Gln Phe Arg Thr Trp Asn Lys Asp Gly Leu Leu Leu Ser Thr Glu
385   390   395   400
Leu Ser Glu Gly Ser Gly Thr Leu Leu Leu Ser Leu Glu Gly Gly Ile
                  405   410   415
Leu Arg Leu Val Ile Gln Lys Met Thr Glu Arg Val Ala Glu Ile Leu
                  420   425   430
Thr Gly Ser Asn Leu Asn Asp Gly Leu Trp His Ser Val Ser Ile Asn
                  435   440   445
Ala Arg Arg Asn Arg Ile Thr Leu Thr Leu Asp Asp Glu Ala Ala Pro
        450   455   460
Pro Ala Pro Asp Ser Thr Trp Val Gln Ile Tyr Ser Gly Asn Ser Tyr
465   470   475   480
Tyr Phe Gly Gly Cys Pro Asp Asn Leu Thr Asp Ser Gln Cys Leu Asn
                  485   490   495
Pro Ile Lys Ala Phe Gln Gly Cys Met Arg Leu Ile Phe Ile Asp Asn
                  500   505   510
Gln Pro Lys Asp Leu Ile Ser Val Gln Gln Gly Ser Leu Gly Asn Phe
                  515   520   525
Ser Asp Leu His Ile Asp Leu Cys Ser Ile Lys Asp Arg Cys Leu Pro
        530   535   540
Asn Tyr Cys Glu His Gly Gly Ser Cys Ser Gln Ser Trp Thr Thr Phe
545   550   555   560
Tyr Cys Asn Cys Ser Asp Thr Ser Tyr Thr Gly Ala Thr Cys His Asn
                  565   570   575
Ser Ile Tyr Glu Gln Ser Cys Glu Val Tyr Arg His Gln Gly Asn Thr
                  580   585   590
Ala Gly Phe Phe Tyr Ile Asp Ser Asp Gly Ser Gly Pro Leu Gly Pro
                  595   600   605
Leu Gln Val Tyr Cys Asn Ile Thr Glu Asp Lys Ile Trp Thr Ser Val
        610   615   620
Gln His Asn Asn Thr Glu Leu Thr Arg Val Arg Gly Ala Asn Pro Glu
625   630   635   640
Lys Pro Tyr Ala Met Ala Leu Asp Tyr Gly Gly Ser Met Glu Gln Leu
                  645   650   655
Glu Ala Val Ile Asp Gly Ser Glu His Cys Glu Gln Glu Val Ala Tyr
                  660   665   670
His Cys Arg Arg Ser Arg Leu Leu Asn Thr Pro Asp Gly Thr Pro Phe
                  675   680   685

30

Thr Trp Trp Ile Gly Arg Ser Asn Glu Arg His Pro Tyr Trp Gly Gly
    690   695   700
Ser Pro Pro Gly Val Gln Gln Cys Glu Cys Gly Leu Asp Glu Ser Cys
705   710   715   720
Leu Asp Ile Gln His Phe Cys Asn Cys Asp Ala Asp Lys Asp Glu Trp
                725   730   735
Thr Asn Asp Thr Gly Phe Leu Ser Phe Lys Asp His Leu Pro Val Thr
                740   745   750
Gln Ile Val Ile Thr Asp Thr Asp Arg Ser Asn Ser Glu Ala Ala Trp
            755   760   765
Arg Ile Gly Pro Leu Arg Cys Tyr Gly Asp Arg Arg Phe Trp Asn Ala
    770   775   780
Val Ser Phe Tyr Thr Glu Ala Ser Tyr Leu His Phe Pro Thr Phe His
785   790   795   800
Ala Glu Phe Ser Ala Asp Ile Ser Phe Phe Phe Lys Thr Thr Ala Leu
                805   810   815
Ser Gly Val Phe Leu Glu Asn Leu Gly Ile Lys Asp Phe Ile Arg Leu
                820   825   830
Glu Ile Ser Ser Pro Ser Glu Ile Thr Phe Ala Ile Asp Val Gly Asn
        835   840   845
Gly Pro Val Glu Leu Val Val Gln Ser Pro Ser Leu Leu Asn Asp Asn
    850   855   860
Gln Trp His Tyr Val Arg Ala Glu Arg Asn Leu Lys Glu Thr Ser Leu
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Gln Val Asp Asn Leu Pro Arg Ser Thr Arg Glu Thr Ser Glu Glu Gly
                885   890   895
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Ser Arg Gln Lys Gly Phe Leu Gly Cys Ile Arg Ser Leu His Leu Asn
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Gly Gln Lys Met Asp Leu Glu Glu Arg Ala Lys Val Thr Ser Gly Val
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Arg Pro Gly Cys Pro Gly His Cys Ser Ser Tyr Gly Ser Ile Cys His
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Asn Gly Gly Lys Cys Val Glu Lys His Asn Gly Tyr Leu Cys Asp Cys
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Thr Asn Ser Pro Tyr Glu Gly Pro Phe Cys Lys Lys Glu Val Ser Ala
                980   985   990
Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met Phe Gln Glu Pro Tyr
            995   1000   1005
Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser Ala Ile Tyr Thr Asp
    1010   1015   1020
Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser Phe Val Thr Thr Gln
1025   1030   1035   1040
Ala Pro Ser Leu Leu Leu Phe Ile Asn Ser Ser Ser Gln Asp Phe Val
                1045   1050   1055
Val Val Leu Leu Cys Lys Asn Gly Ser Leu Gln Val Arg Tyr His Leu
            1060   1065   1070
Asn Lys Glu Glu Thr His Val Phe Thr Ile Asp Ala Asp Asn Phe Ala
            1075   1080   1085
Asn Arg Arg Met His His Leu Lys Ile Asn Arg Glu Gly Arg Glu Leu
    1090   1095   1100
Thr Ile Gln Met Asp Gln Gln Leu Arg Leu Ser Tyr Asn Phe Ser Pro
1105   1110   1115   1120
Glu Val Glu Phe Arg Val Ile Arg Ser Leu Thr Leu Gly Lys Val Thr
                1125   1130   1135

31

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Glu Asn Leu Gly Leu Asp Ser Glu Val Ala Lys Ala Asn Ala Met Gly
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Phe Ala Gly Cys Met Ser Ser Val Gln Tyr Asn His Ile Ala Pro Leu
            1155                1160                1165
Lys Ala Ala Leu Arg His Ala Thr Val Ala Pro Val Thr Val His Gly
            1170                1175                1180
Thr Leu Thr Glu Ser Ser Cys Gly Phe Met Val Asp Ser Asp Val Asn
1185                1190                1195                1200
Ala Val Thr Thr Val His Ser Ser Ser Asp Pro Phe Gly Lys Thr Asp
                1205                1210                1215
Glu Arg Glu Pro Leu Thr Asn Ala Val Arg Ser Asp Ser Ala Val Ile
            1220                1225                1230
Gly Gly Val Ile Ala Val Val Ile Phe Ile Ile Phe Cys Ile Ile Gly
         1235                1240                1245
Ile Met Thr Arg Phe Leu Tyr Gln His Lys Gln Ser His Arg Thr Ser
    1250                1255                1260
Gln Met Lys Glu Lys Glu Tyr Pro Glu Asn Leu Asp Ser Ser Phe Arg
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Phe Ile


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32

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Ile Gly Met Arg Val Glu Val Tyr Gly Cys Ser Tyr Lys Ser Asp Val
            35                  40                  45
Ala Asp Phe Asp Gly Arg Ser Ser Leu Leu Tyr Arg Phe Asn Gln Lys
        50                  55                  60
Leu Met Ser Thr Leu Lys Asp Val Ile Ser Leu Lys Phe Lys Ser Met
65                  70                  75                  80
Gln Gly Asp Gly Val Leu Phe His Gly Glu Gly Gln Arg Gly Asp His
                85                  90                  95
Ile Thr Leu Glu Leu Gln Lys Gly Arg Leu Ala Leu His Leu Asn Leu
            100                 105                 110
Gly Asp Ser Lys Ala Arg Leu Ser Ser Ser Leu Pro Ser Ala Thr Leu
            115                 120                 125
Gly Ser Leu Leu Asp Asp Gln His Trp His Ser Val Leu Ile Glu Arg
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Val Gly Lys Gln Val Asn Phe Thr Val Asp Lys His Thr Gln His Phe
145                      150                      155                      160
Arg Thr Lys Gly Glu Thr Asp Ala Leu Asp Ile Asp Tyr Glu Leu Ser
                   165                      170                      175
Phe Gly Gly Ile Pro Val Pro Gly Lys Pro Gly Thr Phe Leu Lys Lys
                   180                      185                      190
Asn Phe His Gly Cys Ile Glu Asn Leu Tyr Tyr Asn Gly Val Asn Ile
              195                      200                      205
Ile Asp Leu Ala Lys Arg Arg Lys His Gln Ile Tyr Thr Val Gly Asn
         210                      215                      220
Val Thr Phe Ser Cys Ser Glu Pro Gln Ile Val Pro Ile Thr Phe Val
225                      230                      235                      240
Asn Ser Ser Gly Ser Tyr Leu Leu Leu Pro Gly Thr Pro Gln Ile Asp
                   245                      250                      255
Gly Leu Ser Val Ser Phe Gln Phe Arg Thr Trp Asn Lys Asp Gly Leu
                   260                      265                      270
Leu Leu Ser Thr Glu Leu Ser Glu Gly Ser Gly Thr Leu Leu Leu Ser
                   275                      280                      285
Leu Glu Gly Gly Ile Leu Arg Leu Val Ile Gln Lys Met Thr Glu Arg
         290                      295                      300
Val Ala Glu Ile Leu Thr Gly Ser Asn Leu Asn Asp Gly Leu Trp His
305                      310                      315                      320
Ser Val Ser Ile Asn Ala Arg Arg Asn Arg Ile Thr Leu Thr Leu Asp
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Asp Glu Ala Ala Pro Pro Ala Pro Asp Ser Thr Trp Val Gln Ile Tyr
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Ser Gln Cys Leu Asn Pro Ile Lys Ala Phe Gln Gly Cys Met Arg Leu
         370                      375                      380
Ile Phe Ile Asp Asn Gln Pro Lys Asp Leu Ile Ser Val Gln Gln Gly
385                      390                      395                      400
Ser Leu Gly Asn Phe Ser Asp Leu His Ile Asp Leu Cys Ser Ile Lys
                   405                      410                      415
Asp Arg Cys Leu Pro Asn Tyr Cys Glu His Gly Gly Ser Cys Ser Gln
              420                      425                      430
Ser Trp Thr Thr Phe Tyr Cys Asn Cys Ser Asp Thr Ser Tyr Thr Gly
              435                      440                      445
Ala Thr Cys His Asn Ser Ile Tyr Glu Gln Ser Cys Glu Val Tyr Arg
         450                      455                      460
His Gln Gly Asn Thr Ala Gly Phe Phe Tyr Ile Asp Ser Asp Gly Ser
465                      470                      475                      480
Gly Pro Leu Gly Pro Leu Gln Val Tyr Cys Asn Ile Thr Glu Asp Lys
                   485                      490                      495
Ile Trp Thr Ser Val Gln His Asn Asn Thr Glu Leu Thr Arg Val Arg
                   500                      505                      510
Gly Ala Asn Pro Glu Lys Pro Tyr Ala Met Ala Leu Asp Tyr Gly Gly
              515                      520                      525
Ser Met Glu Gln Leu Glu Ala Val Ile Asp Gly Ser Glu His Cys Glu
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Gln Glu Val Ala Tyr His Cys Arg Arg Ser Arg Leu Leu Asn Thr Pro
545                      550                      555                      560
Asp Gly Thr Pro Phe Thr Trp Trp Ile Gly Arg Ser Asn Glu Arg His
                   565                      570                      575
Pro Tyr Trp Gly Gly Ser Pro Pro Gly Val Gln Gln Cys Glu Cys Gly
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34

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              580                    585                    590
Leu Asp Glu Ser Cys Leu Asp Ile Gln His Phe Cys Asn Cys Asp Ala
         595                    600                    605
Asp Lys Asp Glu Trp Thr Asn Asp Thr Gly Phe Leu Ser Phe Lys Asp
    610                    615                    620
His Leu Pro Val Thr Gln Ile Val Ile Thr Asp Thr Asp Arg Ser Asn
625                    630                    635                    640
Ser Glu Ala Ala Trp Arg Ile Gly Pro Leu Arg Cys Tyr Gly Asp Arg
                   645                    650         -          655
Arg Phe Trp Asn Ala Val Ser Phe Tyr Thr Glu Ala Ser Tyr Leu His
                   660                    665                    670
Phe Pro Thr Phe His Ala Glu Phe Ser Ala Asp Ile Ser Phe Phe Phe
         675                    680                    685
Lys Thr Thr Ala Leu Ser Gly Val Phe Leu Glu Asn Leu Gly Ile Lys
         690                    695                    700
Asp Phe Ile Arg Leu Glu Ile Ser Ser Pro Ser Glu Ile Thr Phe Ala
705                    710                    715                    720
Ile Asp Val Gly Asn Gly Pro Val Glu Leu Val Val Gln Ser Pro Ser
                   725                    730                    735
Leu Leu Asn Asp Asn Gln Trp His Tyr Val Arg Ala Glu Arg Asn Leu
                   740                    745                    750
Lys Glu Thr Ser Leu Gln Val Asp Asn Leu Pro Arg Ser Thr Arg Glu
         755                    760                    765
Thr Ser Glu Glu Gly His Phe Arg Leu Gln Leu Asn Ser Gln Leu Phe
         770                    775                    780
Val Gly Gly Thr Ser Ser Arg Gln Lys Gly Phe Leu Gly Cys Ile Arg
785                    790                    795                    800
Ser Leu His Leu Asn Gly Gln Lys Met Asp Leu Glu Glu Arg Ala Lys
                   805                    810                    815
Val Thr Ser Gly Val Arg Pro Gly Cys Pro Gly His Cys Ser Ser Tyr
                   820                    825                    830
Gly Ser Ile Cys His Asn Gly Gly Lys Cys Val Glu Lys His Asn Gly
         835                    840                    845
Tyr Leu Cys Asp Cys Thr Asn Ser Pro Tyr Glu Gly Pro Phe Cys Lys
         850                    855                    860
Lys Glu Val Ser Ala Val Phe Glu Ala Gly Thr Ser Val Thr Tyr Met
865                    870                    875                    880
Phe Gln Glu Pro Tyr Pro Val Thr Lys Asn Ile Ser Leu Ser Ser Ser
                   885                    890                    895
Ala Ile Tyr Thr Asp Ser Ala Pro Ser Lys Glu Asn Ile Ala Leu Ser
                   900                    905                    910
Phe Val Thr Thr Gln Ala Pro Ser Leu Leu Leu Phe Ile Asn Ser Ser
         915                    920                    925
Ser Gln Asp Phe Val Val Val Leu Leu Cys Lys Asn Gly Ser Leu Gln
         930                    935                    940
Val Arg Tyr His Leu Asn Lys Glu Glu Thr His Val Phe Thr Ile Asp
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Ala Asp Asn Phe Ala Asn Arg Arg Met His His Leu Lys Ile Asn Arg
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Glu Gly Arg Glu Leu Thr Ile Gln Met Asp Gln Gln Leu Arg Leu Ser
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Tyr Asn Phe Ser Pro Glu Val Glu Phe Arg Val Ile Arg Ser Leu Thr
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Leu Gly Lys Val Thr Glu Asn Leu Gly Leu Asp Ser Glu Val Ala Lys
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Ala Asn Ala Met Gly Phe Ala Gly Cys Met Ser Ser Val Gln Tyr Asn
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35

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His Ile Ala Pro Leu Lys Ala Ala Leu Arg His Ala Thr Val Ala Pro
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Val Thr Val His Gly Thr Leu Thr Glu Ser Ser Cys Gly Phe Met Val
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Asp Ser Asp Val Asn Ala Val Thr Thr Val His Ser Ser Ser Asp Pro
                1075                1080                1085
Phe Gly Lys Thr Asp Glu Arg Glu Pro Leu Thr Asn Ala Val Arg Ser
           1090                1095                1100
Asp Ser Ala Val Ile Gly Gly Val Ile Ala Val Val Ile Phe Ile Ile
1105                1110                1115                1120
Phe Cys Ile Ile Gly Ile Met Thr Arg Phe Leu Tyr Gln His Lys Gln
                1125                1130                1135
Ser His Arg Thr Ser Gln Met Lys Glu Lys Glu Tyr Pro Glu Asn Leu
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Asp Ser Ser Phe Arg Asn Glu Ile Asp Leu Gln Asn Thr Val Ser Glu
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Cys Lys Arg Glu Tyr Phe Ile
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36
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